0280

2

RAW SEQUENCE LISTING   DATE: 12/12/2001
PATENT APPLICATION: US/10/003,354   TIME: 14:29:56

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\12112001\I003354.raw**   **ENTERED**

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    6 <110> APPLICANT: C. Frank Bennett
    7         Susan M. Freier
    9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-
KINASE, I?
   10         EXPRESSION
   12 <130> FILE REFERENCE: RTS-0348
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C--> 14 <141> CURRENT FILING DATE: 2001-12-06
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   19 <212> TYPE: DNA
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   22 <220> FEATURE:
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   33 <213> ORGANISM: Artificial Sequence
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   50 <221> NAME/KEY: CDS
   51 <222> LOCATION: (401)...(2050)
   53 <400> SEQUENCE: 3
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   55 tgcctcgttt tttttcaga tgtggcttgg tctgggcgca aggtcccagc agccagctta 120
   56 agcttactct tctgtgaaag gggaaagtat cccctgtgga aagcggttaa acttgtggag 180
   57 ggggtgcggg acgtgagttc ttccccatgc caggcgaatg gtgtggcctt gagctggtcc 240
   58 aggagccggc tcgacgtgtc tgagggaggc ccggagggg cggggaggtg gcccacagaa 300
   59 cgcgggttct gtaaagagac gttgggaaga ttcgattccg agaagaggaa gaaccggatt 360
   60 gaaagagagc caggccgctg agggggaggg ggctgctaag atg gcg tcg gcc tcc   415
   61                                                 Met Ala Ser Ala Ser
   62                                                  1                5
   64 tcc ggg ccg tcg tct tcg gtc ggt ttt tca tcc ttt gat ccc gcg gtc  463
   65 Ser Gly Pro Ser Ser Ser Val Gly Phe Ser Ser Phe Asp Pro Ala Val
   66                10                  15                  20
   68 cct tcc tgt acc ttg tcc tca gca tct gga atc aag aga ccc atg gca  511
   69 Pro Ser Cys Thr Leu Ser Ser Ala Ser Gly Ile Lys Arg Pro Met Ala
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72 tct gag gtg cct tat gcc tct ggc atg ccc atc aag aaa ata ggc cat    559
73 Ser Glu Val Pro Tyr Ala Ser Gly Met Pro Ile Lys Lys Ile Gly His
74          40                  45                  50
76 aga agt gtt gat tcc tca gga gag aca aca tat aaa aag aca acc tca    607
77 Arg Ser Val Asp Ser Ser Gly Glu Thr Thr Tyr Lys Lys Thr Thr Ser
78     55                  60                  65
80 tca gcc ttg aaa ggt gcc atc cag tta ggc att acc cac act gtg ggg    655
81 Ser Ala Leu Lys Gly Ala Ile Gln Leu Gly Ile Thr His Thr Val Gly
82 70                  75                  80                  85
84 agc ctg agt acc aaa cca gag cgt gat gtc ctc atg caa gat ttc tac    703
85 Ser Leu Ser Thr Lys Pro Glu Arg Asp Val Leu Met Gln Asp Phe Tyr
86                  90                  95                 100
88 gtg gtt gag agt atc ttc ttt ccc agt gaa ggg agc aac ctg acc cct    751
89 Val Val Glu Ser Ile Phe Phe Pro Ser Glu Gly Ser Asn Leu Thr Pro
90                 105                 110                 115
92 gct cat cac tac aat gac ttt cgt ttc aag acc tat gca cct gtt gcc    799
93 Ala His His Tyr Asn Asp Phe Arg Phe Lys Thr Tyr Ala Pro Val Ala
94         120                 125                 130
96 ttc cgc tac ttc cgg gag cta ttt ggt atc cgg ccc gat gat tac ttg    847
97 Phe Arg Tyr Phe Arg Glu Leu Phe Gly Ile Arg Pro Asp Asp Tyr Leu
98     135                 140                 145
100 tat tcc ctc tgc agt gag ccg ctg att gaa ctc tgt agc tct gga gct   895
101 Tyr Ser Leu Cys Ser Glu Pro Leu Ile Glu Leu Cys Ser Ser Gly Ala
102 150                 155                 160                 165
104 agt ggt tcc cta ttc tat gtg tcc agc gac gat gag ttc att att aag   943
105 Ser Gly Ser Leu Phe Tyr Val Ser Ser Asp Asp Glu Phe Ile Ile Lys
106                 170                 175                 180
108 aca gtc caa cat aaa gag gcg gaa ttt ctg cag aag ctg ctt cca gga   991
109 Thr Val Gln His Lys Glu Ala Glu Phe Leu Gln Lys Leu Leu Pro Gly
110                 185                 190                 195
112 tac tac atg aac ctc aac cag aac cct cgg act ttg ctg cct aaa ttc   1039
113 Tyr Tyr Met Asn Leu Asn Gln Asn Pro Arg Thr Leu Leu Pro Lys Phe
114         200                 205                 210
116 tat gga ctg tac tgt gtg cag gca ggt ggc aag aac att cgg att gtg   1087
117 Tyr Gly Leu Tyr Cys Val Gln Ala Gly Gly Lys Asn Ile Arg Ile Val
118     215                 220                 225
120 gtg atg aac aat ctt tta cca aga tcg gta aaa atg cat atc aaa tat   1135
121 Val Met Asn Asn Leu Leu Pro Arg Ser Val Lys Met His Ile Lys Tyr
122 230                 235                 240                 245
124 gac ctc aaa ggc tca acc tac aaa cgg cgg gct tcc cag aaa gag cga   1183
125 Asp Leu Lys Gly Ser Thr Tyr Lys Arg Arg Ala Ser Gln Lys Glu Arg
126                 250                 255                 260
128 gag aag cct ctt ccc aca ttt aaa gac cta gac ttc tta caa gac atc   1231
129 Glu Lys Pro Leu Pro Thr Phe Lys Asp Leu Asp Phe Leu Gln Asp Ile
130                 265                 270                 275
132 cct gat ggt ctt ttt ttg gat gct gac atg tac aac gct ctc tgt aag   1279
133 Pro Asp Gly Leu Phe Leu Asp Ala Asp Met Tyr Asn Ala Leu Cys Lys
134         280                 285                 290
136 acc ctg cag cgt gac tgt ttg gtg ctg cag agc ttc aag ata atg gat   1327
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137 Thr Leu Gln Arg Asp Cys Leu Val Leu Gln Ser Phe Lys Ile Met Asp
138     295             300             305
140 tac agc ctc ttg atg tca atc cat aat ata gat cat gca caa cga gag  1375
141 Tyr Ser Leu Leu Met Ser Ile His Asn Ile Asp His Ala Gln Arg Glu
142 310             315             320             325
144 ccc tta agc agt gaa aca cag tac tca gtt gat act cga aga ccg gcc  1423
145 Pro Leu Ser Ser Glu Thr Gln Tyr Ser Val Asp Thr Arg Arg Pro Ala
146             330             335             340
148 ccc caa aag gct ctg tat tcc aca gcc atg gaa tcc atc cag gga gag  1471
149 Pro Gln Lys Ala Leu Tyr Ser Thr Ala Met Glu Ser Ile Gln Gly Glu
150             345             350             355
152 gct cga cgg ggt ggt acc atg gag act gat gac cat atg ggt ggc atc  1519
153 Ala Arg Arg Gly Gly Thr Met Glu Thr Asp Asp His Met Gly Gly Ile
154             360             365             370
156 cct gcc cgg aat agt aaa ggg gaa agg ctt ctg ctt tat att ggc atc  1567
157 Pro Ala Arg Asn Ser Lys Gly Glu Arg Leu Leu Leu Tyr Ile Gly Ile
158     375             380             385
160 att gac att cta cag tct tac agg ttt gtt aag aag ttg gag cac tct  1615
161 Ile Asp Ile Leu Gln Ser Tyr Arg Phe Val Lys Lys Leu Glu His Ser
162 390             395             400             405
164 tgg aaa gcc ctg gta cat gac gga gac act gtc tca gtg cat cgc cca  1663
165 Trp Lys Ala Leu Val His Asp Gly Asp Thr Val Ser Val His Arg Pro
166             410             415             420
168 ggc ttc tac gct gaa cgg ttc cag cgc ttc atg tgc aac aca gta ttt  1711
169 Gly Phe Tyr Ala Glu Arg Phe Gln Arg Phe Met Cys Asn Thr Val Phe
170             425             430             435
172 aag aag att ccc ttg aag cct tct cct tcc aaa aag ttt cgg tct ggc  1759
173 Lys Lys Ile Pro Leu Lys Pro Ser Pro Ser Lys Lys Phe Arg Ser Gly
174             440             445             450
176 tca tct ttc tct cgg cga gca ggc tcc agt ggc aac tcc tgc att act  1807
177 Ser Ser Phe Ser Arg Arg Ala Gly Ser Ser Gly Asn Ser Cys Ile Thr
178     455             460             465
180 tac cag cca tcg gtc tct ggg gaa cac aag gca caa gtg aca aca aag  1855
181 Tyr Gln Pro Ser Val Ser Gly Glu His Lys Ala Gln Val Thr Thr Lys
182 470             475             480             485
184 gca gaa gtg gag cca ggc gtt cac ctt ggt cgt cct gat gtt tta cct  1903
185 Ala Glu Val Glu Pro Gly Val His Leu Gly Arg Pro Asp Val Leu Pro
186             490             495             500
188 cag act cca cct ttg gag gaa atc agt gag ggc tcg cct att cct gac  1951
189 Gln Thr Pro Pro Leu Glu Glu Ile Ser Glu Gly Ser Pro Ile Pro Asp
190             505             510             515
192 ccc agt ttc tca cct cta gtt gga gag act ttg caa atg cta act aca  1999
193 Pro Ser Phe Ser Pro Leu Val Gly Glu Thr Leu Gln Met Leu Thr Thr
194             520             525             530
196 agt aca acc ttg gaa aag ctt gaa gtt gca gag tca gag ttc acc cat  2047
197 Ser Thr Thr Leu Glu Lys Leu Glu Val Ala Glu Ser Glu Phe Thr His
198     535             540             545
200 taa gcgcaaagcc tcagaagacc tggaacaaga ttctgccatc tctgtgatcc        2100
204 caagatgtca gcccttgccc cagcaatgct gaattttctt ctacttggtc atcaaaaaag 2160
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207 cctccactcc agagttgggt ggtacggatt ttcaactggc caacccttg cctccactat 2340
208 tgaatttttt tcagacccc attcttcatg ctggaaatgg gattgctgga cttggcagct 2400
209 ttctttcccc tcgtctttga ctaggaaccg gactcttaat ttcctcagga cagactagct 2460
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211 tctgtaaagg tttttggggg ataagggtgt ttaaccacct cccagctttc ttcttctttt 2580
212 tttttctga aaaaggaaa aagcacacag cacacaattt caagccattt tcagatcaga 2640
213 actccagaag tgttgacaag atgcctattc gtagagttcc ctcagaagag ccatggtgtt 2700
214 tatgaagaga agagtagtga ttgctctgcc agaagcagct cctctttaaa ctcctcctct 2760
215 cttgatgaat ttcttaaggc tgaaggaatg aagagagtgg gacatggggt aatctttatc 2820
216 ccttttgtta aaacaggagg cagccatggg ctgggagatc atagcccttc ctaggcagaa 2880
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227 ttttttttcat aatttactat ttatgatgta tttaagtgtt ttattaagga cagagttctg 3540
228 ttaggggtgg gagggaatat ttgagggagg gctgggtctt agggaaagga atggggaagc 3600
229 aacatttta ttaagtgtta ctatttgcct ctactttgta ttgttcagaa atggcaaata 3660
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240 <223> OTHER INFORMATION: PCR Primer
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248 <212> TYPE: DNA
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
253 <223> OTHER INFORMATION: PCR Primer
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256 tcctcttctc ggaatcgaat ct                                             22
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260 <211> LENGTH: 26
261 <212> TYPE: DNA
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
266 <223> OTHER INFORMATION: PCR Probe
268 <400> SEQUENCE: 6
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Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\12112001\I003354.raw**

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286 <211> LENGTH: 20
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288 <213> ORGANISM: Artificial Sequence
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301 <213> ORGANISM: Artificial Sequence
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327 <213> ORGANISM: Artificial Sequence
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334 ctgctgggac cttgcgccca                                          20
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346 <400> SEQUENCE: 12
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VERIFICATION SUMMARY   DATE: 12/12/2001
PATENT APPLICATION: US/10/003,354   TIME: 14:29:57

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\12112001\I003354.raw**

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date